

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/913,800

DATE: 09/05/2001  
 TIME: 13:24:05

Input Set : A:\ES.txt  
 Output Set : N:\CRF3\09052001\I913800.raw

3 <110> APPLICANT: Brett P. Monia  
 4 Lex M. Cowsert  
 6 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-2 EXPRESSION  
 8 <130> FILE REFERENCE: RTSP-0155  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/913,800  
 C--> 11 <141> CURRENT FILING DATE: 2001-08-16  
 13 <150> PRIOR APPLICATION NUMBER: 09/256,465  
 14 <151> PRIOR FILING DATE: 1999-02-23  
 16 <160> NUMBER OF SEQ ID NOS: 47  
 18 <210> SEQ ID NO: 1  
 19 <211> LENGTH: 1599  
 20 <212> TYPE: DNA  
 21 <213> ORGANISM: Homo sapiens  
 23 <220> FEATURE:  
 24 <221> NAME/KEY: CDS  
 25 <222> LOCATION: (88)..(1533)  
 27 <400> SEQUENCE: 1  
 28 gagactgtgc cctgtccacg gtgectctcg catgtcctgc tgcctgagc tgtcccagac 60  
 30 taggtgacag cgtaccacgc tgccacc atg aat gag gtg tct gtc atc aaa 111  
 31 Met Asn Glu Val Ser Val Ile Lys  
 32 1 5  
 34 gaa ggc tgg ctc cac aag cgt ggt gaa tac atc aag acc tgg agg cca 159  
 35 Glu Gly Trp Leu His Lys Arg Gly Glu Tyr Ile Lys Thr Trp Arg Pro  
 36 10 15 20  
 38 cgg tac ttc ctg ctg aag agc gac ggc tcc ttc att ggg tac aag gag 207  
 39 Arg Tyr Phe Leu Leu Lys Ser Asp Gly Ser Phe Ile Gly Tyr Lys Glu  
 40 25 30 35 40  
 42 agg ccc gag gcc cct gat cag act cta ccc tta aac aac ttc tcc 255  
 43 Arg Pro Glu Ala Pro Asp Gln Thr Leu Pro Pro Leu Asn Asn Phe Ser  
 44 45 50 55  
 46 gta gca gaa tgc cag ctg atg aag acc gag agg ccg cga ccc aac acc 303  
 47 Val Ala Glu Cys Gln Leu Met Lys Thr Glu Arg Pro Arg Pro Asn Thr  
 48 60 65 70  
 50 ttt gtc ata cgc tgc ctg cag tgg acc aca gtc atc gag agg acc ttc 351  
 51 Phe Val Ile Arg Cys Leu Gln Trp Thr Thr Val Ile Glu Arg Thr Phe  
 52 75 80 85  
 54 cac gtg gat tct cca gac gag agg gag gag tgg atg cgg gcc atc cag 399  
 55 His Val Asp Ser Pro Asp Glu Arg Glu Glu Trp Met Arg Ala Ile Gln  
 56 90 95 100  
 58 atg gtc gcc aac agc ctc aag cag cgg gcc cca ggc gag gac ccc atg 447  
 59 Met Val Ala Asn Ser Leu Lys Gln Arg Ala Pro Gly Glu Asp Pro Met  
 60 105 110 115 120  
 62 gac tac aag tgt ggc tcc ccc agt gac tcc tcc acg act gag gag atg 495  
 63 Asp Tyr Lys Cys Gly Ser Pro Ser Asp Ser Ser Thr Thr Glu Glu Met  
 64 125 130 135  
 66 gaa gtg gcg gtc agc aag gca cgg gct aaa gtg acc atg aat gac ttc 543  
 67 Glu Val Ala Val Ser Lys Ala Arg Ala Lys Val Thr Met Asn Asp Phe

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68          140          145          150
70  gac tat ctc aaa ctc ctt ggc aag gga acc ttt ggc aaa gtc atc ctg      591
71  Asp Tyr Leu Lys Leu Leu Gly Lys Gly Thr Phe Gly Lys Val Ile Leu
72          155          160          165
74  gtg cgg gag aag gcc act ggc cgc tac tac gcc atg aag atc ctg cga      639
75  Val Arg Glu Lys Ala Thr Gly Arg Tyr Tyr Ala Met Lys Ile Leu Arg
76          170          175          180
78  aag gaa gtc atc att gcc aag gat gaa gtc gct cac aca gtc acc gag      687
79  Lys Glu Val Ile Ile Ala Lys Asp Glu Val Ala His Thr Val Thr Glu
80  185          190          195          200
82  agc cgg gtc ctc cag aac acc agg cac cgg ttc ctc act gcg ctg aag      735
83  Ser Arg Val Leu Gln Asn Thr Arg His Pro Phe Leu Thr Ala Leu Lys
84          205          210          215
86  tat gcc ttc cag acc cac gac cgc ctg tgc ttt gtg atg gag tat gcc      783
87  Tyr Ala Phe Gln Thr His Asp Arg Leu Cys Phe Val Met Glu Tyr Ala
88          220          225          230
90  aac ggg ggt gag ctg ttc ttc cac ctg tcc cgg gag cgt gtc ttc aca      831
91  Asn Gly Gly Glu Leu Phe Phe His Leu Ser Arg Glu Arg Val Phe Thr
92          235          240          245
94  gag gag cgg gcc cgg ttt tat ggt gca gag att gtc tcg gct ctt gag      879
95  Glu Glu Arg Ala Arg Phe Tyr Gly Ala Glu Ile Val Ser Ala Leu Glu
96          250          255          260
98  tac ttg cac tcg cgg gac gtg gta tac cgc gac atc aag ctg gaa aac      927
99  Tyr Leu His Ser Arg Asp Val Val Tyr Arg Asp Ile Lys Leu Glu Asn
100  265          270          275          280
102  ctc atg ctg gac aaa gat ggc cac atc aag atc act gac ttt ggc ctc      975
103  Leu Met Leu Asp Lys Asp Gly His Ile Lys Ile Thr Asp Phe Gly Leu
104          285          290          295
106  tgc aaa gag ggc atc agt gac ggg gcc acc atg aaa acc ttc tgt ggg      1023
107  Cys Lys Glu Gly Ile Ser Asp Gly Ala Thr Met Lys Thr Phe Cys Gly
108          300          305          310
110  acc ccg gag tac ctg gcg cct gag gtg ctg gag gac aat gac tat ggc      1071
111  Thr Pro Glu Tyr Leu Ala Pro Glu Val Leu Glu Asp Asn Asp Tyr Gly
112          315          320          325
114  cgg gcc gtg gac tgg tgg ggg ctg ggt gtg gtc atg tac gag atg atg      1119
115  Arg Ala Val Asp Trp Trp Gly Leu Gly Val Val Met Tyr Glu Met Met
116          330          335          340
118  tgc ggc cgc ctg ccc ttc tac aac cag gac cac gag cgc ctc ttc gag      1167
119  Cys Gly Arg Leu Pro Phe Tyr Asn Gln Asp His Glu Arg Leu Phe Glu
120  345          350          355          360
122  ctc atc ctc atg gaa gag atc cgc ttc ccg cgc acg ctc agc ccc gag      1215
123  Leu Ile Leu Met Glu Glu Ile Arg Phe Pro Arg Thr Leu Ser Pro Glu
124          365          370          375
126  gcc aag tcc ctg ctt gct ggg ctg ctt aag aag gac ccc aag cag agg      1263
127  Ala Lys Ser Leu Leu Ala Gly Leu Leu Lys Lys Asp Pro Lys Gln Arg
128          380          385          390
130  ctt ggt ggg ggg ccc agc gat gcc aag gag gtc atg gag cac agg ttc      1311
131  Leu Gly Gly Gly Pro Ser Asp Ala Lys Glu Val Met Glu His Arg Phe
132          395          400          405

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```

134   ttc ctc agc atc aac tgg cag gac gtg gtc cag aag aag ctc ctg cca   1359
135   Phe Leu Ser Ile Asn Trp Gln Asp Val Val Gln Lys Lys Leu Leu Pro
136       410                               415                               420
138   ccc ttc aaa cct cag gtc acg tcc gag gtc gac aca agg tac ttc gat   1407
139   Pro Phe Lys Pro Gln Val Thr Ser Glu Val Asp Thr Arg Tyr Phe Asp
140   425                               430                               435                               440
142   gat gaa ttt acc gcc cag tcc atc aca atc aca ccc cct gac cgc tat   1455
143   Asp Glu Phe Thr Ala Gln Ser Ile Thr Ile Thr Pro Pro Asp Arg Tyr
144       445                               450                               455
146   gac agc ctg ggc tta ctg gag ctg gac cag cgg acc cac ttc ccc cag   1503
147   Asp Ser Leu Gly Leu Leu Glu Leu Asp Gln Arg Thr His Phe Pro Gln
148       460                               465                               470
150   ttc tcc tac tcg gcc agc atc cgc gag tga gcagtctgcc cagcgagagg   1553
151   Phe Ser Tyr Ser Ala Ser Ile Arg Glu
152       475                               480
154   acgcacgctc gctgccatca ccgctgggtg gttttttacc cctgcc           1599
157 <210> SEQ ID NO: 2
158 <211> LENGTH: 20
159 <212> TYPE: DNA
160 <213> ORGANISM: Artificial Sequence
162 <220> FEATURE:
163 <223> OTHER INFORMATION: PCR Primer ✓
165 <400> SEQUENCE: 2
166   agcagaatgc cagctgatga                                           20
169 <210> SEQ ID NO: 3
170 <211> LENGTH: 20
171 <212> TYPE: DNA
172 <213> ORGANISM: Artificial Sequence
174 <220> FEATURE:
175 <223> OTHER INFORMATION: PCR Primer ✓
177 <400> SEQUENCE: 3
178   gcaggcagcg tatgacaaag                                           20
181 <210> SEQ ID NO: 4
182 <211> LENGTH: 20
183 <212> TYPE: DNA
184 <213> ORGANISM: Artificial Sequence
186 <220> FEATURE:
187 <223> OTHER INFORMATION: PCR Probe ✓
189 <400> SEQUENCE: 4
190   accgagaggc cgcgacccaa                                           20
193 <210> SEQ ID NO: 5
194 <211> LENGTH: 19
195 <212> TYPE: DNA
196 <213> ORGANISM: Artificial Sequence
198 <220> FEATURE:
199 <223> OTHER INFORMATION: PCR Primer ✓
201 <400> SEQUENCE: 5
202   gaaggtgaag gtcggagtc                                           19
205 <210> SEQ ID NO: 6

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## RAW SEQUENCE LISTING

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206 <211> LENGTH: 20  
207 <212> TYPE: DNA  
208 <213> ORGANISM: Artificial Sequence  
210 <220> FEATURE:  
211 <223> OTHER INFORMATION: PCR Primer ✓  
213 <400> SEQUENCE: 6  
214 gaagatggtg atgggatttc 20  
217 <210> SEQ ID NO: 7  
218 <211> LENGTH: 20  
219 <212> TYPE: DNA  
220 <213> ORGANISM: Artificial Sequence  
222 <220> FEATURE:  
223 <223> OTHER INFORMATION: PCR Probe ✓  
225 <400> SEQUENCE: 7  
226 caagcttccc gttctcagcc 20  
229 <210> SEQ ID NO: 8  
230 <211> LENGTH: 18  
231 <212> TYPE: DNA  
232 <213> ORGANISM: Artificial Sequence  
234 <220> FEATURE:  
235 <223> OTHER INFORMATION: Antisense Oligonucleotide ✓  
237 <400> SEQUENCE: 8  
238 tggacagggc acagtctc 18  
241 <210> SEQ ID NO: 9  
242 <211> LENGTH: 18  
243 <212> TYPE: DNA  
244 <213> ORGANISM: Artificial Sequence  
246 <220> FEATURE:  
247 <223> OTHER INFORMATION: Antisense Oligonucleotide ✓  
249 <400> SEQUENCE: 9  
250 gaggcaccgt ggacaggg 18  
253 <210> SEQ ID NO: 10  
254 <211> LENGTH: 18  
255 <212> TYPE: DNA  
256 <213> ORGANISM: Artificial Sequence  
258 <220> FEATURE:  
259 <223> OTHER INFORMATION: Antisense Oligonucleotide ✓  
261 <400> SEQUENCE: 10  
262 tgacagacac ctattca 18  
265 <210> SEQ ID NO: 11  
266 <211> LENGTH: 18  
267 <212> TYPE: DNA  
268 <213> ORGANISM: Artificial Sequence  
270 <220> FEATURE:  
271 <223> OTHER INFORMATION: Antisense Oligonucleotide ✓  
273 <400> SEQUENCE: 11  
274 ctttgatgac agacacct 18  
277 <210> SEQ ID NO: 12  
278 <211> LENGTH: 18

Input Set : A:\ES.txt

Output Set: N:\CRF3\09052001\I913800.raw

279 <212> TYPE: DNA  
280 <213> ORGANISM: Artificial Sequence  
282 <220> FEATURE:  
283 <223> OTHER INFORMATION: Antisense Oligonucleotide ✓  
285 <400> SEQUENCE: 12  
286 ccagccttct ttgatgac 18  
289 <210> SEQ ID NO: 13  
290 <211> LENGTH: 18  
291 <212> TYPE: DNA  
292 <213> ORGANISM: Artificial Sequence  
294 <220> FEATURE:  
295 <223> OTHER INFORMATION: Antisense Oligonucleotide ✓  
297 <400> SEQUENCE: 13  
298 tgtggagcca gccttctt 18  
301 <210> SEQ ID NO: 14  
302 <211> LENGTH: 18  
303 <212> TYPE: DNA  
304 <213> ORGANISM: Artificial Sequence  
306 <220> FEATURE:  
307 <223> OTHER INFORMATION: Antisense Oligonucleotide ✓  
309 <400> SEQUENCE: 14  
310 gatgtattca ccacgctt 18  
313 <210> SEQ ID NO: 15  
314 <211> LENGTH: 18  
315 <212> TYPE: DNA  
316 <213> ORGANISM: Artificial Sequence  
318 <220> FEATURE:  
319 <223> OTHER INFORMATION: Antisense Oligonucleotide ✓  
321 <400> SEQUENCE: 15  
322 gtcttgatgt attcacca 18  
325 <210> SEQ ID NO: 16  
326 <211> LENGTH: 18  
327 <212> TYPE: DNA  
328 <213> ORGANISM: Artificial Sequence  
330 <220> FEATURE:  
331 <223> OTHER INFORMATION: Antisense Oligonucleotide ✓  
333 <400> SEQUENCE: 16  
334 ccaatgaagg agccgtcg 18  
337 <210> SEQ ID NO: 17  
338 <211> LENGTH: 18  
339 <212> TYPE: DNA  
340 <213> ORGANISM: Artificial Sequence  
342 <220> FEATURE:  
343 <223> OTHER INFORMATION: Antisense Oligonucleotide ✓  
345 <400> SEQUENCE: 17  
346 ctacggagaa gttgttta 18  
349 <210> SEQ ID NO: 18  
350 <211> LENGTH: 18  
351 <212> TYPE: DNA

VERIFICATION SUMMARY

DATE: 09/05/2001

PATENT APPLICATION: US/09/913,800

TIME: 13:24:06

Input Set : A:\ES.txt

Output Set: N:\CRF3\09052001\I913800.raw

L:10 M:270 C: Current Application Number differs, Replaced Application Number

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date